

RAW SEQUENCE LISTING

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Application Serial Number: 10/679,694

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/679,694

DATE: 10/18/2004

TIME: 09:28:11

Input Set : N:\Crf3\RULE60\10679694.raw.txt

Output Set: N:\CRF4\10182004\J679694.raw

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Margolis, Benjamin L.

(ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATMENT
OF BREAST CANCER

(iii) NUMBER OF SEQUENCES: 21

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: PENNIE & EDMONDS LLP
(B) STREET: 1155 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 10036-2711

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/10/679,694

(B) FILING DATE: 07-Oct-2003

(C) CLASSIFICATION: 435

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Coruzzi, Laura A.

(B) REGISTRATION NUMBER: 30,742

(C) REFERENCE/DOCKET NUMBER: 7683-053

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 790-9090

(B) TELEFAX: (212) 869-9741/8864

(C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Gly Xaa Gly Xaa Xaa Gly

1 5

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

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65 (B) TYPE: amino acid
66 (C) STRANDEDNESS: single
67 (D) TOPOLOGY: unknown
69 (ii) MOLECULE TYPE: peptide
71 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
73 Val Ala Val Lys
74 1
77 (2) INFORMATION FOR SEQ ID NO: 3:
79 (i) SEQUENCE CHARACTERISTICS:
80 (A) LENGTH: 5 amino acids
81 (B) TYPE: amino acid
82 (C) STRANDEDNESS: single
83 (D) TOPOLOGY: unknown
85 (ii) MOLECULE TYPE: peptide
87 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
W--> 89 Gly Met Xaa Tyr Leu
90 1 5
93 (2) INFORMATION FOR SEQ ID NO: 4:
95 (i) SEQUENCE CHARACTERISTICS:
96 (A) LENGTH: 9 amino acids
97 (B) TYPE: amino acid
98 (C) STRANDEDNESS: single
99 (D) TOPOLOGY: unknown
101 (ii) MOLECULE TYPE: peptide
103 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
105 Ile His Arg Asp Leu Ala Ala Arg Asn
106 1 5
109 (2) INFORMATION FOR SEQ ID NO: 5:
111 (i) SEQUENCE CHARACTERISTICS:
112 (A) LENGTH: 6 amino acids
113 (B) TYPE: amino acid
114 (C) STRANDEDNESS: single
115 (D) TOPOLOGY: unknown
117 (ii) MOLECULE TYPE: peptide
119 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
121 Lys Trp Met Ala Pro Glu
122 1 5
125 (2) INFORMATION FOR SEQ ID NO: 6:
127 (i) SEQUENCE CHARACTERISTICS:
128 (A) LENGTH: 6 amino acids
129 (B) TYPE: amino acid
130 (C) STRANDEDNESS: single
131 (D) TOPOLOGY: unknown
133 (ii) MOLECULE TYPE: peptide
135 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
137 Lys Trp Thr Ala Pro Glu
138 1 5
141 (2) INFORMATION FOR SEQ ID NO: 7:
143 (i) SEQUENCE CHARACTERISTICS:

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```

144      (A) LENGTH: 6 amino acids
145      (B) TYPE: amino acid
146      (C) STRANDEDNESS: single
147      (D) TOPOLOGY: unknown
149      (ii) MOLECULE TYPE: peptide
151      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
153      Phe Trp Tyr Ala Pro Glu
154      1           5
157 (2) INFORMATION FOR SEQ ID NO: 8:
159      (i) SEQUENCE CHARACTERISTICS:
160          (A) LENGTH: 7 amino acids
161          (B) TYPE: amino acid
162          (C) STRANDEDNESS: single
163          (D) TOPOLOGY: unknown
165      (ii) MOLECULE TYPE: peptide
167      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
169      Ser Asp Val Trp Ser Phe Gly
170      1           5
173 (2) INFORMATION FOR SEQ ID NO: 9:
175      (i) SEQUENCE CHARACTERISTICS:
176          (A) LENGTH: 334 amino acids
177          (B) TYPE: amino acid
178          (C) STRANDEDNESS: single
179          (D) TOPOLOGY: unknown
181      (ii) MOLECULE TYPE: protein
183      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
185      Arg Asp Ser Ser Arg Leu Cys Val Val Lys Val Tyr Ser Glu Asp Gly
186      1           5           10           15
188      Ala Cys Arg Ser Val Glu Val Ala Ala Gly Ala Thr Ala Arg His Val
189      20           25           30
191      Cys Glu Met Leu Val Gln Arg Ala His Ala Leu Ser Asp Glu Ser Trp
192      35           40           45
194      Gly Leu Val Glu Ser His Pro Tyr Leu Ala Leu Glu Arg Gly Leu Glu
195      50           55           60
197      Asp His Glu Phe Val Val Glu Val Gln Glu Ala Trp Pro Val Gly Gly
198      65           70           75           80
200      Asp Ser Arg Phe Ile Phe Arg Lys Asn Phe Ala Lys Tyr Glu Leu Phe
201      85           90           95
203      Lys Ser Pro Pro His Thr Leu Phe Pro Glu Lys Met Val Ser Ser Cys
204      100          105          110
206      Leu Asp Ala Gln Thr Gly Ile Ser His Glu Asp Leu Ile Gln Asn Phe
207      115          120          125
209      Leu Asn Ala Gly Ser Phe Pro Glu Ile Gln Gly Phe Leu Gln Leu Arg
210      130          135          140
212      Gly Ser Gly Arg Gly Ser Gly Arg Lys Leu Trp Lys Arg Phe Phe Cys
213      145          150          155          160
215      Phe Leu Arg Arg Ser Gly Leu Tyr Tyr Ser Thr Lys Gly Thr Ser Lys
216      165          170          175
218      Asp Pro Arg His Leu Gln Tyr Val Ala Asp Val Asn Glu Ser Asn Val

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```

219          180          185          190
221  Tyr Val Val Thr Gln Gly Arg Lys Leu Tyr Gly Met Pro Thr Asp Phe
222          195          200          205
224  Gly Phe Cys Val Lys Pro Asn Lys Leu Arg Asn Gly His Lys Gly Leu
225          210          215          220
227  His Ile Phe Cys Ser Glu Asp Glu Gln Ser Arg Thr Cys Trp Leu Ala
228          225          230          235          240
230  Ala Phe Arg Leu Phe Lys Tyr Gly Val Gln Leu Tyr Lys Asn Tyr Gln
231          245          250          255
233  Gln Ala Gln Ser Arg His Leu Arg Leu Ser Tyr Leu Gly Ser Pro Pro
234          260          265          270
236  Leu Arg Ser Val Ser Asp Asn Thr Leu Val Ala Met Asp Phe Ser Gly
237          275          280          285
239  His Ala Gly Arg Val Ile Asp Asn Pro Arg Glu Ala Leu Ser Ala Ala
240          290          295          300
242  Met Glu Glu Ala Gln Ala Trp Arg Lys Lys Thr Asn His Arg Leu Ser
243          305          310          315          320
245  Leu Pro Thr Thr Cys Ser Gly Ser Ser Leu Ser Ala Ala Ile
246          325          330

```

249 (2) INFORMATION FOR SEQ ID NO: 10:

251 (i) SEQUENCE CHARACTERISTICS:
252 (A) LENGTH: 348 amino acids
253 (B) TYPE: amino acid
254 (C) STRANDEDNESS: single
255 (D) TOPOLOGY: unknown

257 (ii) MOLECULE TYPE: protein

259 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```

261  Lys Glu Ala Lys Val Thr Lys Ile Phe Val Lys Phe Phe Val Glu Asp
262          1          5          10          15
264  Gly Glu Ala Leu Gln Leu Leu Ile Asp Glu Arg Trp Thr Val Ala Asp
265          20          25          30
267  Thr Leu Lys Gln Leu Ala Glu Lys Asn His Ile Ala Leu Met Glu Asp
268          35          40          45
270  His Cys Ile Val Glu Glu Tyr Pro Glu Leu Tyr Ile Lys Arg Val Tyr
271          50          55          60
273  Glu Asp His Glu Lys Val Val Glu Asn Ile Gln Met Trp Val Gln Asp
274          65          70          75          80
276  Ser Pro Asn Lys Leu Tyr Phe Met Arg Arg Pro Asp Lys Tyr Ala Phe
277          85          90          95
279  Ile Ser Arg Pro Glu Leu Tyr Leu Leu Thr Pro Lys Thr Ser Asp His
280          100         105         110
282  Met Glu Ile Pro Ser Gly Asp Gln Trp Thr Ile Asp Val Lys Gln Lys
283          115         120         125
285  Phe Val Ser Glu Tyr Phe His Arg Glu Pro Val Val Pro Pro Glu Met
286          130         135         140
288  Glu Gly Phe Leu Tyr Leu Lys Ser Asp Gly Arg Lys Ser Trp Lys Lys
289          145         150         155         160
291  His Tyr Phe Val Leu Arg Pro Ser Gly Leu Tyr Tyr Ala Pro Lys Ser
292          165         170         175

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Input Set : N:\Crf3\RULE60\10679694.raw.txt
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```

294 Lys Lys Pro Thr Thr Lys Asp Leu Thr Cys Leu Met Asn Leu His Ser
295 180 185 190
297 Asn Gln Val Tyr Thr Gly Ile Gly Trp Glu Lys Lys Tyr Lys Ser Pro
298 195 200 205
300 Thr Pro Trp Cys Ile Ser Ile Lys Leu Thr Ala Leu Gln Met Lys Arg
301 210 215 220
303 Ser Gln Phe Ile Lys Tyr Ile Cys Ala Glu Asp Glu Met Thr Phe Lys
304 225 230 235 240
306 Lys Trp Leu Val Ala Leu Arg Ile Ala Lys Asn Gly Ala Glu Leu Leu
307 245 250 255
309 Glu Asn Tyr Glu Arg Ala Cys Gln Ile Arg Arg Glu Thr Leu Gly Pro
310 260 265 270
312 Ala Ser Ser Met Ser Ala Ala Ser Ser Ser Thr Ala Ile Ser Glu Val
313 275 280 285
315 Pro His Ser Leu Ser His His Gln Arg Thr Pro Ser Val Ala Ser Ser
316 290 295 300
318 Ile Gln Leu Ser Ser His Met Met Asn Asn Pro Thr His Pro Leu Ser
319 305 310 315 320
321 Val Asn Val Arg Asn Gln Ser Pro Ala Ser Phe Ser Val Asn Ser Cys
322 325 330 335
324 Gln Gln Ser His Pro Ser Arg Thr Ser Ala Lys Leu
325 340 345

```

328 (2) INFORMATION FOR SEQ ID NO: 11:

330 (i) SEQUENCE CHARACTERISTICS:

331 (A) LENGTH: 111 amino acids
 332 (B) TYPE: amino acid
 333 (C) STRANDEDNESS: single
 334 (D) TOPOLOGY: unknown

336 (ii) MOLECULE TYPE: protein

338 (ix) FEATURE:

339 (A) NAME/KEY: Modified-site
 340 (B) LOCATION: 1, 25-27, 32, 46, 47, 49, 52, 54, 72
 341 75, 77, 93, 95, 105, 107, 108 and 111

342 (D) OTHER INFORMATION: /label= Xaa
 343 /note= "Xaa at these positions = Hydrophobic
 344 residues"

346 (ix) FEATURE:

347 (A) NAME/KEY: Modified-site
 348 (B) LOCATION: 2, 21, 23 and 101
 349 (D) OTHER INFORMATION: /label= Xaa

350 /note= "Xaa at these positions = Basic residues"

352 (ix) FEATURE:

353 (A) NAME/KEY: Modified-site
 354 (B) LOCATION: 3, 7, 9, 11-19, 22, 28-31, 36-42, 44, 48
 355 50, 51, 53, 55-70, 74, 76, 78-90, 92, 94

356 96-98, 106 109 and 110

357 (D) OTHER INFORMATION: /label= Xaa

358 /note= "Xaa at these positions = Non-consensus
 359 residues"

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/18/2004
PATENT APPLICATION: US/10/679,694 TIME: 09:28:12

Input Set : N:\Crf3\RULE60\10679694.raw.txt
Output Set: N:\CRF4\10182004\J679694.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos.2,4,5
Seq#:3; Xaa Pos.3
Seq#:11; Xaa Pos.1,2,3,7,9,11,12,13,14,15,16,17,18,19,21,22,23,24,25,26,27
Seq#:11; Xaa Pos.28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,44,46,47,48
Seq#:11; Xaa Pos.49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67
Seq#:11; Xaa Pos.68,69,70,72,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88
Seq#:11; Xaa Pos.89,90,91,92,93,94,95,96,97,98,99,100,101,102,103,105,106
Seq#:11; Xaa Pos.107,108,109,110,111
Seq#:12; Xaa Pos.7,11,12,13,14,15,16,17,22,28,29,31,33,35,38,39,40,41,42,46
Seq#:12; Xaa Pos.47,50,51,52,58,59,60,61,62,63,64,65,66,67,68,70,72,74,76
Seq#:12; Xaa Pos.77,78,80,81,82,83,84,85,86,87,88,89,90,91,92,96,98,109,110
Seq#:14; Xaa Pos.2,3,5
Seq#:15; Xaa Pos.1,3,5,7
Seq#:16; Xaa Pos.1,3,4,8,9

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/679,694

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TIME: 09:28:12

Input Set : N:\CrF3\RULE60\10679694.raw.txt
Output Set: N:\CRF4\10182004\J679694.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vi)
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:57 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:89 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
M:341 Repeated in SeqNo=11
L:550 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
M:341 Repeated in SeqNo=12
L:618 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:668 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0